SEQUENCE LISTING

<110> Guertler, Lutz G.
       Eberle, Josef
       Brunn, Albrecht V.
       Knapp, Stefan
       Hauser, Hans-Peter

<120> RETROVIRUS FROM HIV GROUP AND ITS USE

<130> 05495.0001-04

<140> 09/109,916
<141> 1998-07-02

<150> DE P 42 33 646.5
<151> 1992-10-06

<150> DE P 42 35 718.7
<151> 1992-10-22

<150> DE P 42 44 541.8
<151> 1992-12-30

<150> DE P 43 18 186.4
<151> 1993-06-01

<160> 67

<170> PatentIn Ver. 2.0

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<220>
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<210> 8

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<400> 8
agcacattgt actgatatct a                                                   21


<210> 9
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<210> 10
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ccatgcaaat gttaaaagag ac                                                  22


<210> 12
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<210> 14
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<212> DNA
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<220>
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<210> 15
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aatggagcca gtagatccta   20

<210> 16
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<212> DNA
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<220>
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<210> 17
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 17

gagccctgga agcatccagg   20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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ggagatgcct aaggcttttg   20

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<220>
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tgttccttgg gttcttg   17

<210> 20
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<220>
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<220>
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<210> 23
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<210> 24
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<212> DNA
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<210> 25
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
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tcaggatcca tgggcagtct agcagaagaa g


<210> 26
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<212> DNA
<213> Artificial Sequence

<220>
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<210> 27
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<220>
<223> Description of Artificial Sequence: primer

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<210> 29
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 30
gctgacattt atcacagctg gctac                                    25


<210> 31
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 32
<211> 22
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
agtccctgac atgctgtcat ca   22

<210> 33
<211> 22
<212> DNA
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<220>
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<400> 33
gtggagggga atttttctac tg   22

<210> 34
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<220>
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<400> 34
cctgctgctc ccaagaaccc aagg   24

<210> 35
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<220>
<223> Description of Artificial Sequence: primer

<400> 35
agcagcagga agcactatgg   20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 36
gagttttcca gagcaacccc   20

<210> 37

<211> 195
<212> DNA
<213> Human immunodeficiency virus

<220>
<221> CDS
<222> (3)..(194)

<400> 37
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gc gca gcg gca aca gcg ctg acg gta cgg acc cac agt gta ctg aag     47
   Ala Ala Ala Thr Ala Leu Thr Val Arg Thr His Ser Val Leu Lys
   1               5                   10                  15

ggt ata gtg caa cag cag gac aac ctg ctg aga gcg ata cag gcc cag     95
Gly Ile Val Gln Gln Gln Asp Asn Leu Leu Arg Ala Ile Gln Ala Gln
               20                  25                  30

caa cac ttg ctg agg tta tct gta tgg ggt att aga caa ctc cga gct    143
Gln His Leu Leu Arg Leu Ser Val Trp Gly Ile Arg Gln Leu Arg Ala
               35                  40                  45

cgc ctg caa gcc tta gaa acc ctt ata cag aat cag caa cgc cta aac    191
Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn
           50                  55                  60

                                                                   195
cta t
Leu
```

<210> 38
<211> 195
<212> DNA
<213> Human immunodeficiency virus

<400> 38
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ataggtttag gcgttgctga ttctgtataa gggtttctaa ggcttgcagg cgagctcgga  60

gttgtctaat accccataca gataacctca gcaagtgttg ctgggcctgt atcgctctca 120

gcaggttgtc ctgctgttgc actataccct tcagtacact gtgggtccgt accgtcagcg 180

                                                                  195
ctgttgccgc tgcgc
```

<210> 39
<211> 64
<212> PRT
<213> Human immunodeficiency virus

<400> 39
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Ala Ala Ala Thr Ala Leu Thr Val Arg Thr His Ser Val Leu Lys Gly
1               5                   10                  15

Ile Val Gln Gln Gln Asp Asn Leu Leu Arg Ala Ile Gln Ala Gln Gln
               20                  25                  30

His Leu Leu Arg Leu Ser Val Trp Gly Ile Arg Gln Leu Arg Ala Arg
               35                  40                  45
```

Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn Leu
    50   55   60

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 40
cagaatcagc aacgcctaaa cc   22

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
gccctgtctt attcttctag g   21

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 42
gcctgcaagc cttagaaacc   20

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 43
gcactatacc cttcagtaca ctg   23

<210> 44
<211> 1057
<212> DNA
<213> Human immunodeficiency virus

<220>

<221> CDS
<222> (3)..(1055)

<400> 44
aa atg tca aga cca ata ata aac att cac acc cct cac agg gaa aaa   47
   Met Ser Arg Pro Ile Ile Asn Ile His Thr Pro His Arg Glu Lys
    1   5   10   15

aga cga gta gga ttg gga atg cta ttc ttg ggg gtg cta agt gca gca   95
Arg Arg Val Gly Leu Gly Met Leu Phe Leu Gly Val Leu Ser Ala Ala
                20   25   30

ggt agc act atg ggc gca gcg gca aca gcg ctg acg gta cgg acc cac   143
Gly Ser Thr Met Gly Ala Ala Ala Thr Ala Leu Thr Val Arg Thr His
            35   40   45

agt gta ctg aag ggt ata gtg caa cag cag gac aac ctg ctg aga gcg   191
Ser Val Leu Lys Gly Ile Val Gln Gln Gln Asp Asn Leu Leu Arg Ala
        50   55   60

ata cag gcc cag caa cac ttg ctg agg tta tct gta tgg ggt att aga   239
Ile Gln Ala Gln Gln His Leu Leu Arg Leu Ser Val Trp Gly Ile Arg
    65   70   75

caa ctc cga gct cgc ctg caa gcc tta gaa acc ctt ata cag aat cag   287
Gln Leu Arg Ala Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln
 80   85   90   95

caa cgc cta aac cta tgg ggc tgt aaa gga aaa cta atc tgt tac aca   335
Gln Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu Ile Cys Tyr Thr
                100   105   110

tca gta aaa tgg aac aca tca tgg tca gga gga tat aat gat gac agt   383
Ser Val Lys Trp Asn Thr Ser Trp Ser Gly Gly Tyr Asn Asp Asp Ser
            115   120   125

att tgg gac aac ctt aca tgg cag caa tgg gac caa cac ata aac aat   431
Ile Trp Asp Asn Leu Thr Trp Gln Gln Trp Asp Gln His Ile Asn Asn
        130   135   140

gta agc tcc att ata tat gat gaa ata caa gca gca caa gac caa cag   479
Val Ser Ser Ile Ile Tyr Asp Glu Ile Gln Ala Ala Gln Asp Gln Gln
    145   150   155

gaa aag aat gta aaa gca ttg ttg gag cta gat gaa tgg gcc tct ctt   527
Glu Lys Asn Val Lys Ala Leu Leu Glu Leu Asp Glu Trp Ala Ser Leu
160   165   170   175

tgg aat tgg ttt gac ata act aaa tgg ttg tgg tat ata aaa ata gct   575
Trp Asn Trp Phe Asp Ile Thr Lys Trp Leu Trp Tyr Ile Lys Ile Ala
                180   185   190

ata atc ata gtg gga gca cta ata ggt ata aga gtt atc atg ata gta   623
Ile Ile Ile Val Gly Ala Leu Ile Gly Ile Arg Val Ile Met Ile Val
            195   200   205

```
ctt aat cta gtg aag aac att agg cag gga tat caa ccc ctc tcg ttg   671
Leu Asn Leu Val Lys Asn Ile Arg Gln Gly Tyr Gln Pro Leu Ser Leu
        210             215             220

cag atc cct gtc cca cac cgg cag gaa gca gaa acg cca gga aga aca   719
Gln Ile Pro Val Pro His Arg Gln Glu Ala Glu Thr Pro Gly Arg Thr
    225             230             235

gga gaa gaa ggt gga gaa gga gac agg ccc aag tgg aca gcc ttg cca   767
Gly Glu Glu Gly Gly Glu Gly Asp Arg Pro Lys Trp Thr Ala Leu Pro
240             245             250             255

cca gga ttc ttg caa cag ttg tac acg gat ctc agg aca ata atc ttg   815
Pro Gly Phe Leu Gln Gln Leu Tyr Thr Asp Leu Arg Thr Ile Ile Leu
            260             265             270

tgg act tac cac ctc ttg agc aac tta ata tca ggg atc cgg agg ctg   863
Trp Thr Tyr His Leu Leu Ser Asn Leu Ile Ser Gly Ile Arg Arg Leu
        275             280             285

atc gac tac ctg gga ctg gga ctg tgg atc ctg gga caa aag aca att   911
Ile Asp Tyr Leu Gly Leu Gly Leu Trp Ile Leu Gly Gln Lys Thr Ile
        290             295             300

gaa gct tgt aga ctt tgt gga gct gta atg caa tat tgg cta caa gaa   959
Glu Ala Cys Arg Leu Cys Gly Ala Val Met Gln Tyr Trp Leu Gln Glu
    305             310             315

ttg aaa aat agt gct aca aac ctg ctt gat act att gca gtg tca gtt   1007
Leu Lys Asn Ser Ala Thr Asn Leu Leu Asp Thr Ile Ala Val Ser Val
320             325             330             335

gcc aat tgg act gac ggc atc atc tta ggt cta caa aga ata gga caa   1055
Ala Asn Trp Thr Asp Gly Ile Ile Leu Gly Leu Gln Arg Ile Gly Gln
            340             345             350

gg                                                                1057
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<210> 45
<211> 1057
<212> DNA
<213> Human immunodeficiency virus

<400> 45
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gcaatagtat caagcaggtt tgtagcacta ttttcaatt cttgtagcca atattgcatt 120

acagctccac aaagtctaca agcttcaatt gtcttttgtc ccaggatcca cagtcccagt 180

cccaggtagt cgatcagcct ccggatccct gatattaagt tgctcaagag gtggtaagtc 240

cacaagatta ttgtcctgag atccgtgtac aactgttgca agaatcctgg tggcaaggct 300

gtccacttgg gcctgtctcc ttctccacct tcttctcctg ttcttcctgg cgtttctgct 360

tcctgccggt gtgggacagg gatctgcaac gagagggtt gatatccctg cctaatgttc 420
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ttcactagat taagtactat catgataact cttataccta ttagtgctcc cactatgatt  480

atagctattt ttatatacca caaccattta gttatgtcaa accaattcca aagagaggcc  540

cattcatcta gctccaacaa tgcttttaca ttctttcct gttggtcttg tgctgcttgt  600

attccatcat atataatgga gcttacattg tttatgtgtt ggtcccattg ctgccatgta  660

aggttgtccc aaatactgtc atcattatat cctcctgacc atgatgtgtt ccattttact  720

gatgtgtaac agattagttt tcctttacag ccccataggt ttaggcgttg ctgattctgt  780

ataagggttt ctaaggcttg caggcgagct cggagttgtc taatacccca tacagataac  840

ctcagcaagt gttgctgggc ctgtatcgct ctcagcaggt tgtcctgctg ttgcactata  900

cccttcagta cactgtgggt ccgtaccgtc agcgctgttg ccgctgcgcc catagtgcta  960

cctgctgcac ttagcacccc caagaatagc attcccaatc ctactgctct ttttcccctg  1020

tgagggtgt gaatgtttat tattggtctt gacattt                            1057
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<210> 46
<211> 351
<212> PRT
<213> Human immunodeficiency virus

<400> 46
Met Ser Arg Pro Ile Ile Asn Ile His Thr Pro His Arg Glu Lys Arg
  1               5                  10                  15

Arg Val Gly Leu Gly Met Leu Phe Leu Gly Val Leu Ser Ala Ala Gly
               20              25                  30

Ser Thr Met Gly Ala Ala Ala Thr Ala Leu Thr Val Arg Thr His Ser
          35              40                  45

Val Leu Lys Gly Ile Val Gln Gln Gln Asp Asn Leu Leu Arg Ala Ile
      50              55                  60

Gln Ala Gln Gln His Leu Leu Arg Leu Ser Val Trp Gly Ile Arg Gln
  65              70              75                  80

Leu Arg Ala Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln
              85              90                  95

Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu Ile Cys Tyr Thr Ser
          100             105                 110

Val Lys Trp Asn Thr Ser Trp Ser Gly Gly Tyr Asn Asp Asp Ser Ile
          115             120                 125

Trp Asp Asn Leu Thr Trp Gln Gln Trp Asp Gln His Ile Asn Asn Val
          130             135                 140
```

Ser Ser Ile Ile Tyr Asp Glu Ile Gln Ala Ala Gln Asp Gln Gln Glu
145   150   155   160

Lys Asn Val Lys Ala Leu Leu Glu Leu Asp Glu Trp Ala Ser Leu Trp
                165   170   175

Asn Trp Phe Asp Ile Thr Lys Trp Leu Trp Tyr Ile Lys Ile Ala Ile
            180   185   190

Ile Ile Val Gly Ala Leu Ile Gly Ile Arg Val Ile Met Ile Val Leu
        195   200   205

Asn Leu Val Lys Asn Ile Arg Gln Gly Tyr Gln Pro Leu Ser Leu Gln
    210   215   220

Ile Pro Val Pro His Arg Gln Glu Ala Glu Thr Pro Gly Arg Thr Gly
225   230   235   240

Glu Glu Gly Gly Glu Gly Asp Arg Pro Lys Trp Thr Ala Leu Pro Pro
            245   250   255

Gly Phe Leu Gln Gln Leu Tyr Thr Asp Leu Arg Thr Ile Ile Leu Trp
            260   265   270

Thr Tyr His Leu Leu Ser Asn Leu Ile Ser Gly Ile Arg Arg Leu Ile
        275   280   285

Asp Tyr Leu Gly Leu Gly Leu Trp Ile Leu Gly Gln Lys Thr Ile Glu
    290   295   300

Ala Cys Arg Leu Cys Gly Ala Val Met Gln Tyr Trp Leu Gln Glu Leu
305   310   315   320

Lys Asn Ser Ala Thr Asn Leu Leu Asp Thr Ile Ala Val Ser Val Ala
            325   330   335

Asn Trp Thr Asp Gly Ile Ile Leu Gly Leu Gln Arg Ile Gly Gln
            340   345   350

<210> 47
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 47
ctagcagtgg cgcccgaaca gg   22

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 48
aatgaggaag cwgcagawtg gga   23

<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 49
tcccawtctg cwgcttcctc att   23

<210> 50
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 50
ccaaggggaa gtgacatagc aggaac   26

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 51
cgttgttcag aattcaaacc c   21

<210> 52
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 52
tccctaaaaa attagcctgt c   21

<210> 53
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 53
aaacctccaa ttcccccta   19

<210> 54
<211> 39
<212> PRT
<213> Human immunodeficiency virus

<400> 54
Cys Ile Arg Glu Gly Ile Ala Glu Val Gln Asp Ile Tyr Thr Gly Pro
  1   5   10   15

Met Arg Trp Arg Ser Met Thr Leu Lys Arg Ser Asn Asn Thr Ser Pro
             20   25   30

Arg Ser Arg Val Ala Tyr Cys
         35

<210> 55
<211> 41
<212> PRT
<213> Human immunodeficiency virus

<400> 55
Cys Ile Arg Glu Gly Ile Ala Glu Val Gln Asp Leu His Thr Gly Pro
  1   5   10   15

Leu Arg Trp Arg Ser Met Thr Leu Lys Lys Ser Ser Asn Ser His Thr
             20   25   30

Gln Pro Arg Ser Lys Val Ala Tyr Cys
         35   40

<210> 56
<211> 9793
<212> DNA
<213> Human immunodeficiency virus

<400> 56
ctggatgggt taatttactc ccataagaga gcagaaatcc tggatctctg gatatatcac 60

actcagggat tcttccctga ttggcagtgt tacacaccgg gaccaggacc tagattccca 120

ctgacatttg gatggttgtt taaactggta ccagtgtcag cagaagaggc agagagactg 180

ggtaatacaa atgaagatgc tagtcttcta catccagctt gtaatcatgg agctgaggat 240

gcacacgggg agatactaaa atggcagttt gatagatcat taggcttaac acatatagcc 300

ctgcaaaagc acccagagct cttcccccaag taactgacac tgcgggactt tccagactgc 360

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tgacactgcg gggactttcc agcgtgggag ggataagggg cggttcgggg agtggctaac 420

cctcagatgc tgcatataag cagctgcttt ccgcttgtac cgggtcttag ttagaggacc 480

aggtctgagc ccgggagctc cctggcctct agctgaaccc gctgcttaac gctcaataaa 540

gcttgccttg agtgagaagc agtgtgtgct catctgttca accctggtgt ctagagatcc 600

ctcagatcac ttagactgaa gcagaaaatc tctagcagtg gcgcccgaac agggacgcga 660

aagtgaaagt ggaaccaggg aagaaaacct ccgacgcaac gggctcggct tagcggagtg 720

cacctgctaa gaggcgagag gaactcacaa gagggtgagt aaatttgctg gcggtggcca 780

gacctagggg aagggcgaag tccctagggg aggaagatgg gtgcgagagc gtctgtgttg 840

acagggagta aattggatgc atgggaacga attaggttaa ggccaggatc taaaaaggca 900

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aagacagggt cagaggacct gaaatctctc tggaacgcaa tagcagtact ctggtgcgtt 1080

cacaacagat ttgacatccg agatacacag caggcaatac aaaagttaaa ggaagtaatg 1140

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actttaaatg catgggtaaa ggcagtagaa gagaaggcct ttaaccctga aattattcct 1320

atgtttatgg cattatcaga aggggctgtc ccctatgata tcaataccat gctgaatgcc 1380

ataggggac accaaggggc tttacaagtg ttgaaggaag taatcaatga ggaagcagca 1440

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<212> DNA
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<211> 498
<212> PRT
<213> Human immunodeficiency virus

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Glu Arg Ile Arg Leu Arg Pro Gly Ser Lys Lys Ala Tyr Arg Leu Lys
                20                  25                  30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Arg Tyr Ala Cys Asn Pro
            35                  40                  45

Gly Leu Leu Glu Thr Ala Glu Gly Thr Glu Gln Leu Leu Gln Gln Leu
        50                  55                  60
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Glu Pro Ala Leu Lys Thr Gly Ser Glu Asp Leu Lys Ser Leu Trp Asn
65   70   75   80

Ala Ile Ala Val Leu Trp Cys Val His Asn Arg Phe Asp Ile Arg Asp
              85   90   95

Thr Gln Gln Ala Ile Gln Lys Leu Lys Glu Val Met Ala Ser Arg Lys
          100   105   110

Ser Ala Glu Ala Ala Lys Glu Glu Thr Ser Pro Arg Gln Thr Ser Gln
      115   120   125

Asn Tyr Pro Ile Val Thr Asn Ala Gln Gly Gln Met Val His Gln Ala
      130   135   140

Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Ala Val Glu Glu Lys
145   150   155   160

Ala Phe Asn Pro Glu Ile Ile Pro Met Phe Met Ala Leu Ser Glu Gly
              165   170   175

Ala Val Pro Tyr Asp Ile Asn Thr Met Leu Asn Ala Ile Gly Gly His
          180   185   190

Gln Gly Ala Leu Gln Val Leu Lys Glu Val Ile Asn Glu Glu Ala Ala
      195   200   205

Glu Trp Asp Arg Thr His Pro Pro Ala Met Gly Pro Leu Pro Pro Gly
      210   215   220

Gln Ile Arg Glu Pro Thr Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr
225   230   235   240

Gln Gln Glu Gln Ile Ile Trp Thr Thr Arg Gly Ala Asn Ser Ile Pro
              245   250   255

Val Gly Asp Ile Tyr Arg Lys Trp Ile Val Leu Gly Leu Asn Lys Met
          260   265   270

Val Lys Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro
          275   280   285

Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg
      290   295   300

Ala Glu Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu
305   310   315   320

Leu Val Gln Asn Ser Asn Pro Asp Cys Lys Gln Ile Leu Lys Ala Leu
              325   330   335

Gly Pro Glu Ala Thr Leu Glu Glu Met Met Val Ala Cys Gln Gly Val
          340   345   350

Gly Gly Pro Thr His Lys Ala Lys Ile Leu Ala Glu Ala Met Ala Ser
          355   360   365

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Gly Gln Asn Pro Asn Arg Lys Gly Pro Ile Lys Cys Phe Asn Cys Gly
385                 390             395             400

Lys Glu Gly His Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Arg Gly
            405             410             415

Cys Trp Lys Cys Gly Gln Glu Gly His Gln Met Lys Asp Cys Lys Asn
        420             425             430

Gly Arg Gln Ala Asn Phe Leu Gly Lys Tyr Trp Pro Pro Gly Gly Thr
    435             440             445

Arg Pro Gly Asn Tyr Val Gln Lys Gln Val Ser Pro Ser Ala Pro Pro
    450             455             460

Met Glu Glu Ala Val Lys Glu Gln Glu Asn Gln Ser Gln Lys Gly Asp
465             470             475             480

Gln Glu Glu Leu Tyr Pro Phe Ala Ser Leu Lys Ser Leu Phe Gly Thr
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Asp Gln
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<212> PRT
<213> Human immunodeficiency virus

<400> 60
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Glu Arg Ile Arg Leu Arg Pro Gly Ser Lys Lys Ala Tyr Arg Leu Lys
            20              25              30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Arg Tyr Ala Tyr Asn Pro
        35              40              45

Gly Leu Leu Glu Thr Ala Glu Gly Thr Glu Gln Leu Leu Gln Gln Leu
    50              55              60

Glu Pro Ala Leu Lys Thr Gly Ser Glu Asp Leu Lys Ser Leu Trp Asn
65              70              75              80

Ala Ile Ala Val Leu Trp Cys Val His Asn Arg Phe Asp Ile Arg Asp
            85              90              95

Thr Gln Gln Ala Ile Gln Lys Leu Lys Glu Val Met Ala Ser Arg Lys
            100             105             110

Ser Ala Glu Ala Ala Lys Glu Glu Thr Ser Ser Thr Gln Ala Ser Gln
    115             120             125
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Asn Tyr Pro Ile Val Thr Asn Ala Gln Gly Gln Met Val His Gln Ala
  130   135   140

Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Ala Val Glu Glu Lys
145   150   155   160

Ala Phe Asn Pro Glu Ile Ile Pro Met Phe Met Ala Leu Ser Glu Gly
          165   170   175

Ala Val Pro Tyr Asp Ile Asn Thr Met Leu Asn Ala Ile Gly Gly His
          180   185   190

Gln Gly Ala Leu Gln Val Leu Lys Glu Val Ile Asn Glu Glu Ala Ala
      195   200   205

Asp Trp Asp Arg Thr His Pro Pro Ala Met Gly Pro Leu Pro Pro Gly
  210   215   220

Gln Ile Arg Glu Pro Thr Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr
225   230   235   240

Gln Gln Glu Gln Ile Ile Trp Thr Thr Arg Gly Ala Asn Ser Ile Pro
          245   250   255

Val Gly Asp Ile Tyr Arg Lys Trp Ile Val Leu Gly Leu Asn Lys Met
          260   265   270

Val Lys Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro
      275   280   285

Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg
  290   295   300

Ala Glu Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu
305   310   315   320

Val Val Gln Asn Ser Asn Pro Asp Cys Lys Gln Ile Leu Lys Ala Leu
          325   330   335

Gly Pro Gly Ala Thr Leu Glu Glu Met Met Val Ala Cys Gln Gly Val
          340   345   350

Gly Gly Pro Thr His Lys Ala Lys Ile Leu Ala Glu Ala Met Ala Ser
      355   360   365

Ala Gln Gln Asp Leu Lys Gly Gly Tyr Thr Ala Val Phe Met Gln Arg
  370   375   380

Gly Gln Asn Pro Asn Arg Lys Gly Pro Ile Lys Cys Phe Asn Cys Gly
385   390   395   400

Lys Glu Gly His Ile Ala Lys Asn Cys Arg Ala Pro Arg Arg Arg Gly
          405   410   415

Tyr Trp Lys Cys Gly Gln Glu Gly His Gln Met Lys Asp Cys Lys Asn
      420   425   430

Gly Arg Gln Ala Asn Phe Leu Gly Lys Tyr Trp Pro Pro Gly Gly Thr
        435   440   445

Arg Pro Ala Asn Tyr Val Gln Lys Gln Val Ser Pro Ser Ala Pro Pro
        450   455   460

Met Glu Glu Ala Val Lys Glu Gln Glu Asn Gln Asn Gln Lys Gly Asp
465   470   475   480

Gln Glu Glu Leu Tyr Pro Phe Ala Ser Leu Lys Ser Leu Phe Gly Thr
                485   490   495

Asp Gln

<210> 61
<211> 35
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 61
Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly
  1   5   10   15

Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp
                20   25   30

Asn Ala Ser
        35

<210> 62
<211> 35
<212> PRT
<213> Human immunodeficiency virus

<400> 62
Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn
  1   5   10   15

Leu Trp Gly Cys Lys Gly Lys Leu Ile Cys Tyr Thr Ser Val Lys Trp
                20   25   30

Asn Thr Ser
        35

<210> 63
<211> 25
<212> PRT
<213> Human immunodeficiency virus

<400> 63
Trp Gly Ile Arg Gln Leu Arg Ala Arg Leu Gln Ala Leu Glu Thr Leu
  1   5   10   15

Ile Gln Asn Gln Gln Arg Leu Asn Leu
                20   25

<210> 64
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 64
ccataatatt cagcagaact ag   22

<210> 65
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 65
gctgattctg tataaggg   18

<210> 66
<211> 36
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 66
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gln Arg
  1   5   10   15

Gly Pro Gly Arg Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg
                20   25   30

Gln Ala His Cys
            35

<210> 67
<211> 36
<212> PRT
<213> Human immunodeficiency virus type 2

<400> 67
Cys Lys Arg Pro Gly Asn Lys Ile Val Lys Gln Ile Met Leu Met Ser
  1   5   10   15

Gly His Val Phe His Ser His Tyr Gln Pro Ile Asn Lys Arg Pro Arg
                20   25   30

Gln Ala Trp Cys
            35